PEROXISOME-ASSOCIATED POLYPEPTIDE...
Bernard Knoops, et al.
Appl. No.: 09/486167   Atty Docket: DECLE30.001APC

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B18 mRNA (arbitrary units)

FIG. 1

PEROXISOME-ASSOCIATED POLYPEPTIDE...
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FIG. 2

PEROXISOME-ASSOCIATED POLYPEPTIDE...
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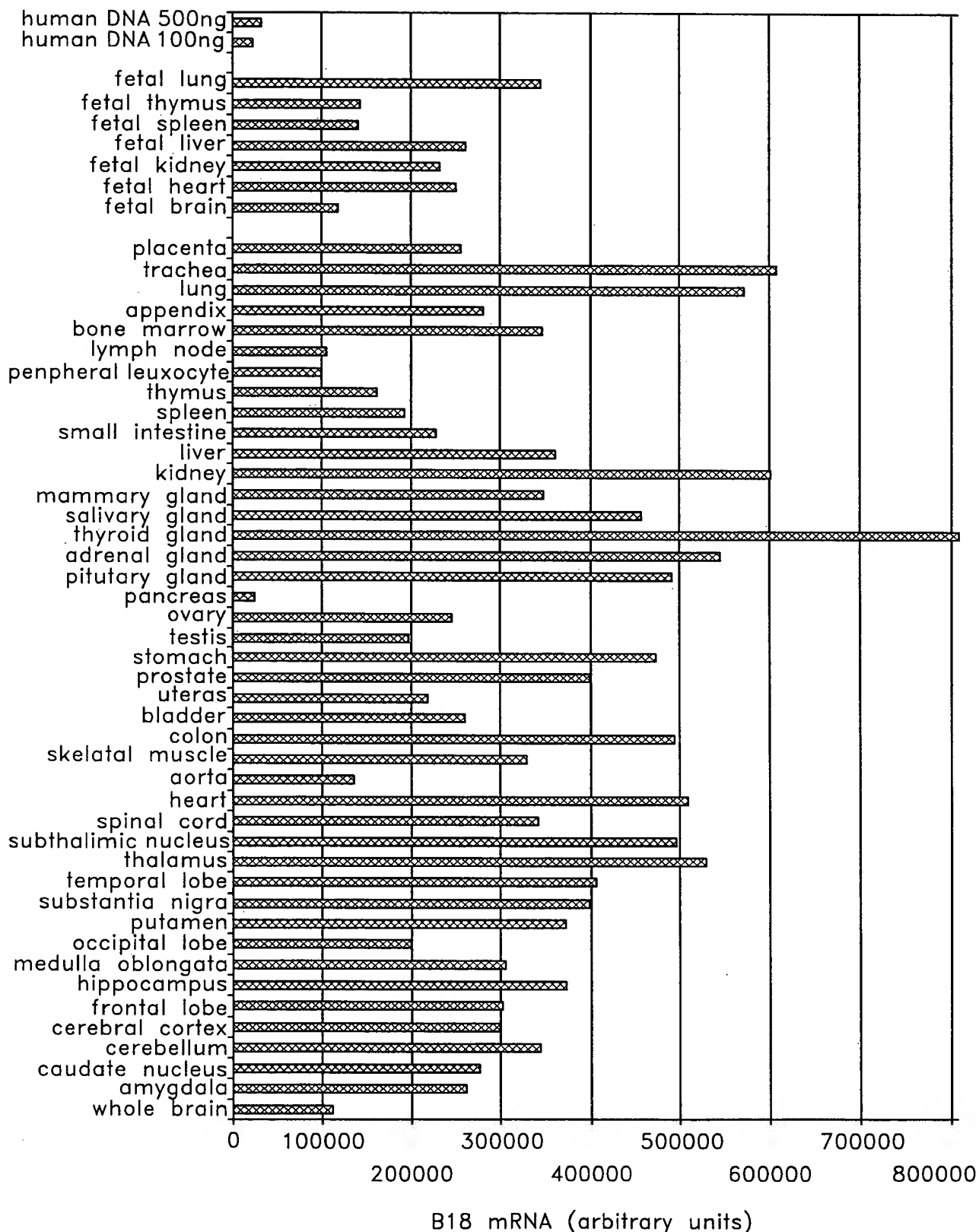*Appl. No.: 09/486167 Atty Docket: DECLE30.001APC*

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FIG. 3

PEROXISOME-ASSOCIATED POLYPEPTIDE...
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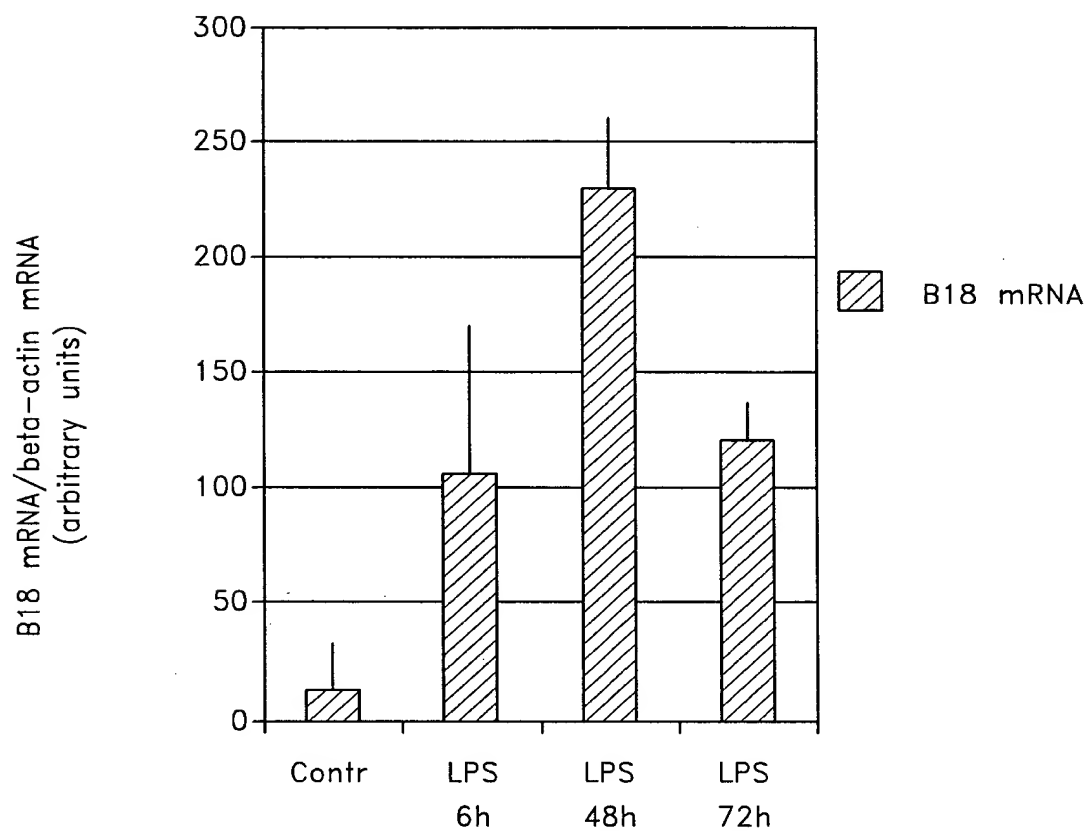*Appl. No.: 09/486167   Atty Docket: DECLE30.001APC*

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Gene (chromosome 11q12–13)

EXONS

mRNAs

800
670
668
530

Proteins
ATPase–β   A.O.   PRX
17kDa
12.3kDa
12.3kDa
7.7kDa

FIG. 4

PEROXISOME-ASSOCIATED POLYPEPTIDE...
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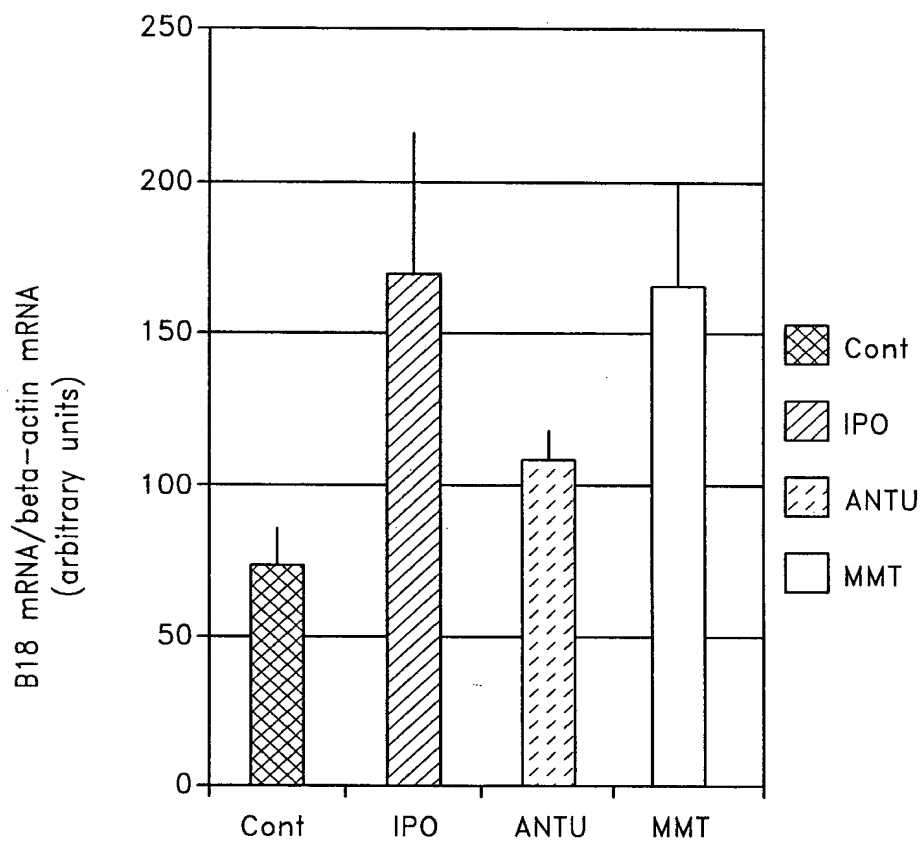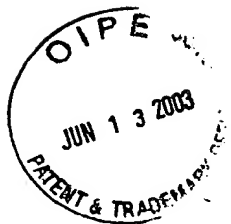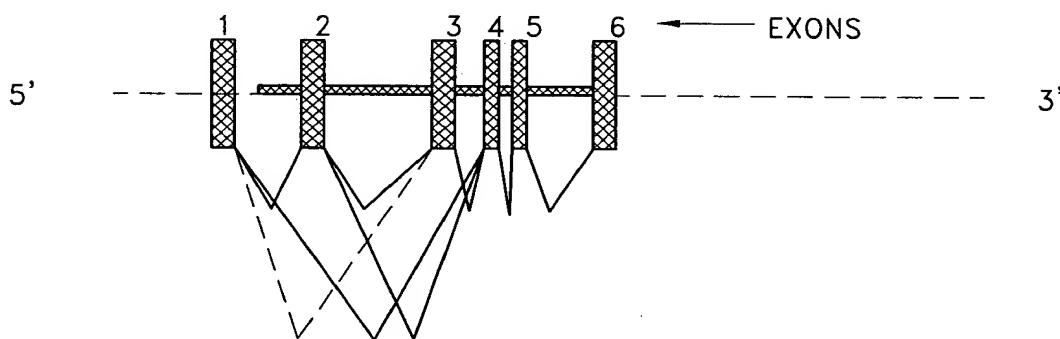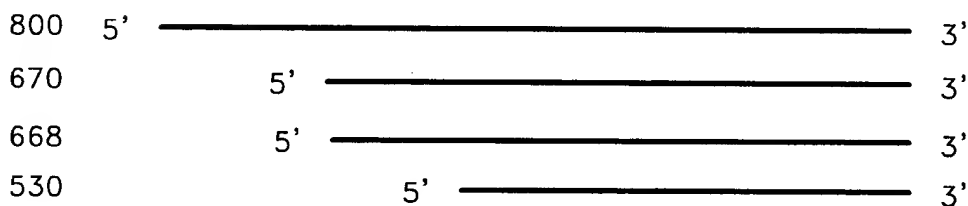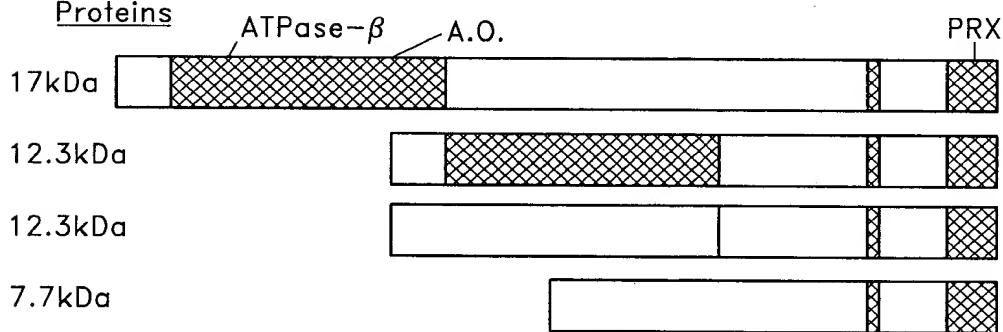CLUSTAL V alignment of human and rat B18 amino acid sequences
(Identity: 908, Homology: 97.5%):

B18hum MAPIKVGDAIPAVEVFEGEPGNKVNLAELFKGKKGVLFGVPGAFTPGCSK = SEQIDNO1
B18rat MAPIKVGDTIPSVEVFEGEPGKKVNLAELFKDKKGVLFGVPGAFTPGCSK
        ******* .** .********* .********* .*****************

B18hum THLPGFVEQAEALKAKGVQVVACLSVNDAFVTGEWGRAHKAEGKVRLLAD
B18rat THLPGFVEQAGALKAKGAQVVACLSVNDVFVTAEWGRAHQAEGKVQLLAD
        ********** ****** ********** *** .****** .***** .****

B18hum PTGAFGKETDLLLDDSLVSIFGNRRLKRFSMVVQDGIVKALNVEPDGTGL
B18rat PTGAFGKETDLLLDDSLVSLFGNRRLKRFSMVIDKGVVKALNVEPDGTGL
        ******************* .************ .. * .*************

B18hum TCSLAPNIISQL
B18rat TCSLAPNILSQL
        ******** .***
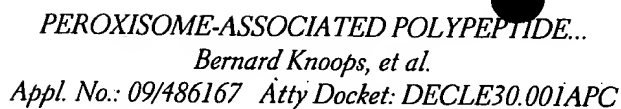

CLUSTAL V alignment of human and mouse B18 amino acid sequences
(Identity: 91%, Homology: 96%)

B18hum   MAPIKVGDAIPAVEVFEGEPGNKVNLAELFKGKKGVLFGVPGAFTPGCSK
B18mouse MAPIKVGDAIPSVEVFEGEPGKKVNLAELFKGKKGVLFGVPGAFTPGCSK
          ********** .******** .****************************

B18hum   THLPGFVEQAEALKAKGVQVVACLSVNDAFVTGEWGRAHKAEGKVRLLAD
B18mouse THLPGFVEQAGALKAKGAQVVACLSVNDVFVIEEWGRAHQAEGKVRLLAD
          ********** ****** ********** **   ****** .*********

B18hum   PTGAFGKETDLLLDDSLVSIFGNRRLKRFSMVVQDGIVKALNVEPDGTGL
B18mouse PTGAFGKATDLLLDDSLVSLFGNRRLKRFSMVIDNGIVKALNVEPDGTGL
          ******* *********** .*********** ... ***************

B18hum   TCSLAPNIISQL
B18mouse TCSLAPNILSQL
          ******** .***

CLUSTAL V alignment of human and rat cDNA sequences (identity:
612/780,78.5%):

B18hum GCCAGGAGGCGGAGTGGAAGTGGCCGTGGGGCGGGTATGGGACTAGCTGG
        --------------TG--------CGTC-------------CTAGGCAG
                      **   ***   ****   *

B18hum CGTGTGCGCCCTGAGACGCTCAGCGGGCTATATACTCGTCGGTGGGGCCG
B18rat CATA---GCC---GGA---TCGGTGCTCCGTGCATCGGCTACTTGGAC-
        * *   ***   **. ** * *   *   *   *   * ** *

B18hum GCGGTCAGTCTGCGGCAGCGGCAGCAAGACGGTGCAGTGAAGGAGAGTGG
B18rat -------GTGCGTGGCAGGCAGAGCAGGCCGG---AAAGGAGCAGGTTGG
          ** * ***** **** * *** *   * * ** ** ***

FIG. 5A

```
B18hum  GCGTCTGGCGGGGTCCGCAGTTTCAGCAGAGCCGCTGCAGCCATGGCCCC
B18rat  GAGTGTGGTGGGGCCCGCAGCTTCAGCAGTGCCGCGGTGACTATGGCCCC
        * ** *** **** ****** ******* ***** *   * ********


B18hum  AATCAAGGTGGGAGATGCCATCCCAGCAGTGGAGGTGTTTGAAGGGGAGC
B18rat  GATCAAGGTGGGAGACACCATTCCCTCAGTGGAGGTATTTGAAGGGGAAC
        ************** **** ** ********** *********** *


B18hum  CAGGGAACAAGGTGAACCTGGCAGAGCTGTTCAAGGGCAAGAAGGGTGTG
B18rat  CTGGAAAGAAGGTGAACTTGGCAGAGCTGTTCAAGGACAAGAAAGGTGTT
        * ** ** ********* ****************** ****** *****


B18hum  CTGTTTGGAGTTCCTGGGGCCTTCACCCCTGGATGTTCCAAGACACACCT
B18rat  TTGTTTGGAGTCCCTGGGGCATTTACACCTGGCTGTTCCAAGACCCATCT
        ********* ******* ** ** ***** ********** ** **


B18hum  GCCAGGGTTTGTGGAGCAGGCTGAGGCTCTGAAGGCCAAGGGAGTCCAGG
B18rat  GCCTGGGTTTGTGGAGCAAGCCGGAGCTCTGAAGGCCAAGGGAGCACAAG
        *** ************** ** *   ****************** ** *


B18hum  TGGTGGCCTGTCTGAGTGTTAATGATGCCTTTGTGACTGGCGAGTGGGGC
B18rat  TGGTGGCCTGTCTGAGTGTTAATGATGTCTTCGTGACTGCAGAGTGGGGT
        *************************** *** ******* ** *******


B18hum  CGAGCCCACAAGGCGGAAGGCAAGGTTCGGCTCCTGGCTGATCCCACTGG
B18rat  CGAGCCCACCAGGCAGAAGGCAAGGTTCAGCTCCTGGCTGACCCCACTGG
        ********* **** ************* ************ ********


B18hum  GGCCTTTGGGAAGGAGACAGACTTATTACTAGATGATTCGCTGGTGTCCA
B18rat  AGCTTTTGGAAAGGAGACAGATTTACTACTAGATGATTCTTTGGTGTCTC
        ** ***** ********** *** ************* *******


B18hum  TCTTTGGGAATCGACGTCTCAAGAGGTTCTCCATGGTGGTACAGGATGGC
B18rat  TCTTTGGGAATCGTCGGCTAAAAAGGTTCTCCATGGTGATAGACAAGGGC
        ************* ** ** ** ************** ** *  * ***


B18hum  ATAGTGAAGGCCCTGAATGTGGAACCAGATGGCACAGGCCTCACCTGCAG
B18rat  GTAGTAAAGGCACTGAACGTGGAGCCGGATGGCACAGGCCTCACCTGCAG
        **** ***** ***** ***** ** *************************


B18hum  CCTGGCACCCAATATCATCTCACAGCTCTGAGGCCCTGGGCCAGATTACT
B18rat  CCTGGCCCCCAACATCCTCTCACAACTCTGAGGCCCTGA-CCAGA--ATG
        ****** ***** *** ******* ************* *****   *


B18hum  TCCTCCACCCCTCCCTATCTCACCTGCCCAGCCCTGTGCTGG-GGCCCTG
B18rat  TCCTCTGACTCTCCC-ATCTCCTCCACCCAGCTCTGGGCCAAAGGCCCAG
        *****   * ***** ***** *****  ****** ****   ***** *


B18hum  CA------------------ATTGGAATG-----TTGGCCAGATTTCTGC
B18rat  TACCTCCTTACCTGAGGGCCACTGGAATGGAACCTTGACAATATTTCTGC
        ' *                  * *******    *** * * ********


B18hum  AATAAACACTTGTGGTTTGCGGAAAAAAA-------------
B18rat  AATAAACAGTT-TAATTTGTGAAAAAAAAAAAAAAAAAAAAAA
        ******** ** *   **** * *******
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FIG. 5B

CLUSTAL V alignment of human and mouse cDNA sequences
(identity:552/675, 81.8%)

```
B18hum    GCCAGGAGGCGGAGTGGAAGTGGCCGTGGGGCGGGTATGGGACTAGCTGG
B18mouse  --------------------------------------------------

B18hum    CGTGTGCGCCCTGAGACGCTCAGCGGGCTATATACTCGTCGGTGGGGCCG
B18mouse  ----------------TGCTCCGTG----------CATCGACGTGCTTG
                          ****  *  *          *  ***  *  *    *
B18hum    GCGGTCAGTCTGCGGCAGCGGCAGCAAGACGGTGCAGTGAAGGAGAGTGG
B18mouse  GCAGGCAG-------------AGCAGGCCGG---AAAGAAGCAGGTTGG
          **  *  ***          ****  *  ***   *   ****  **   ***
B18hum    GCGTCTGGCGGGGTCCGCAGTTTCAGCAGAGCCGCTGCAGCCATGGCCCC
B18mouse  GAGTGTGGCGGAGCCCGCAGCTTCAGCAGCTCCGCGGTGACCATGGCCCC
          *  **  ******  *  ******  *******    ****  *   *********
B18hum    AATCAAGGTGGGAGATGCCATCCCAGCAGTGGAGGTGTTTGAAGGGGAGC
B18mouse  GATCAAGGTGGGAGATGCCATTCCCTCAGTGGAGGTATTTGAAGGGGAAC
          ****************** **  ********* ********** *
B18hum    CAGGGAACAAGGTGAACCTGGCAGAGCTGTTCAAGGGCAAGAAGGGTGTG
B18mouse  CGGGAAAGAAGGTGAACTTGGCAGAGCTGTTCAAGGGCAAGAAAGGTGTT
          *  **  **  ********  ************************  *  *****
B18hum    CTGTTTGGAGTTCCTGGGGCCTTCACCCCTGGATGTTCCAAGACACACCT
B18mouse  TTGTTTGGAGTCCCTGGGGCATTTACACCTGGCTGTTCTAAGACCCACCT
          **********  *******  **  **  *****  *****  *****  *****
B18hum    GCCAGGGTTTGTGGAGCAGGCTGAGGCTCTGAAGGCCAAGGGAGTCCAGG
B18mouse  GCCTGGGTTTGTGGAGCAAGCTGGAGCTCTGAAGGCTAAGGGAGCGCAGG
          ***  **************  ****  ***********  *******   ****
B18hum    TGGTGGCCTGTCTGAGTGTTAATGATGCCTTTGTGACTGGCGAGTGGGGC
B18mouse  TGGTGGCCTGTCTGAGCGTTAATGACGTCTTTGTGATTGAAGAGTGGGGT
          ****************  *******  *  *******  **   *******
B18hum    CGAGCCCACAAGGCGGAAGGCAAGGTTCGGCTCCTGGCTGATCCCACTGG
B18mouse  CGAGCCCACCAGGCAGAAGGCAAGGTTCGGCTCCTGGCTGACCCCACTGG
          *********  ****  ********************************  *******
B18hum    GGCCTTTGGGAAGGAGACAGACTTATTACTAGATGATTCGCTGGTGTCCA
B18mouse  AGCCTTTGGGAAGGCGACAGACTTATTATTGGATGATTCTTTGGTGTCTC
          **********  ************  ****  *  *******    *******
B18hum    TCTTTGGGAATCGACGTCTCAAGAGGTTCTCCATGGTGGTACAGGATGGC
B18mouse  TCTTTGGGAATCGTCGGCTGAAAAGGTTCTCCATGGTGATAGACAACGGC
          *************  **  **  ** *************** **  *   *  ***
B18hum    ATAGTGAAGGCCCTGAATGTGGAACCAGATGGCACAGGCCTCACCTGCAG
B18mouse  ATAGTGAAGGCACTGAACGTGGAGCCAGATGGCACAGGCCTCACCTGCAG
          **********  *****  *****  *************************
B18hum    CCTGGCACCCAATATCATCTCACAGCTCTGAGGCCCTGGGCCAGATTACT
B18mouse  CCTGGCCCCCAACATCCTCTCCCAACTCTGAGGCCCTGG-CCAGATG---
          ******  *****  ***  ****  **  *************  ******
B18hum    TCCTCCACCCCTCCCTATCTCACCTGCCCAGCCCTGTGCTGGGGCCCTGC
B18mouse  TCCTCTGACTCTCCC-ATCTCTCCCACCCGGCTCT------AGGCC----
          *****  *  *****  *****  ***  **  **         ****
B18hum    AATTGGAATGTTGGCCAGATTTCTGCAATAAACACTTGTGGTTTGCGGAA
B18mouse  ----AAAGGCTCGGTACCTCCTTACTGGGAGC-CACGT-----------
              **  *  *   *  *      *  *      *  *  **
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FIG. 5C